

#6

OICE

## RAW SEQUENCE LISTING

DATE: 08/14/2001

PATENT APPLICATION: US/09/819,930

TIME: 09:37:10

Input Set : A:\Ma278412.app

Output Set: N:\CRF3\08142001\I819930.raw

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3 <110> APPLICANT: FARWICK, MIKE
4      MOCKEL, BETTINA
5      PFEFFERLE, WALTER
7 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING THE PTSH GENE
9 <130> FILE REFERENCE: MAS/21123/278412
11 <140> CURRENT APPLICATION NUMBER: 09/819,930
12 <141> CURRENT FILING DATE: 2001-03-29
14 <150> PRIOR APPLICATION NUMBER: 09/755,187
15 <151> PRIOR FILING DATE: 2001-01-08
17 <150> PRIOR APPLICATION NUMBER: DE 100 01 101.2
18 <151> PRIOR FILING DATE: 2000-01-13
20 <160> NUMBER OF SEQ ID NOS: 6
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 480
26 <212> TYPE: DNA
27 <213> ORGANISM: Corynebacterium glutamicum
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (163)..(429)
32 <223> OTHER INFORMATION: ptsH wild-type gene
34 <400> SEQUENCE: 1
35 ggacattggtt ttgtcttcg gtaacgtggc aaaacgaaca atgtctcact agactaaagt 60
37 gagatcgaca ttaaattccc tcccttgggg ggtttaacta acaaatcgct gcgcctaata 120
39 ccgttcggat taacggcgta gcaacacgaa aggacacttt cc atg gct tcc aag 174
40                                     Met Ala Ser Lys
41                                     1
43 act gta acc gtc ggt tcc tcc gtt ggc ctg cac gca cgt cca gca tcc 222
44 Thr Val Thr Val Gly Ser Ser Val Gly Leu His Ala Arg Pro Ala Ser
45 5 10 15 20
47 atc atc gct gaa gcg gct gct gag tac gac gac gaa atc ttg ctg acc 270
48 Ile Ile Ala Glu Ala Ala Ala Glu Tyr Asp Asp Glu Ile Leu Leu Thr
49 25 30 35
51 ctg gtt ggc tcc gat gat gac gaa gag acc gac gcg tcc tct tcc ctc 318
52 Leu Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala Ser Ser Ser Leu
53 40 45 50
55 atg atc atg gcg ctg ggc gca gag cac ggc aac gaa gtt acc gtc acc 366
56 Met Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu Val Thr Val Thr
57 55 60 65
59 tcc gac aac gct gaa gct gtt gag aag atc gct gcg ctt atc gca cag 414
60 Ser Asp Asn Ala Glu Ala Val Glu Lys Ile Ala Ala Leu Ile Ala Gln
61 70 75 80
63 gac ctt gac gct gag taaacaacgc tctgcttggt aaaagctcgt tagaagcttg 469
64 Asp Leu Asp Ala Glu
65 85
67 ttaaaagcgg t 480
70 <210> SEQ ID NO: 2

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71 <211> LENGTH: 89
72 <212> TYPE: PRT
73 <213> ORGANISM: Corynebacterium glutamicum
75 <400> SEQUENCE: 2
76 Met Ala Ser Lys Thr Val Thr Val Gly Ser Ser Val Gly Leu His Ala
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79 Arg Pro Ala Ser Ile Ile Ala Glu Ala Ala Glu Tyr Asp Asp Glu
80           20           25           30
82 Ile Leu Leu Thr Leu Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala
83           35           40           45
85 Ser Ser Ser Leu Met Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu
86           50           55           60
88 Val Thr Val Thr Ser Asp Asn Ala Glu Ala Val Glu Lys Ile Ala Ala
89   65           70           75           80
91 Leu Ile Ala Gln Asp Leu Asp Ala Glu
92           85
95 <210> SEQ ID NO: 3
96 <211> LENGTH: 480
97 <212> TYPE: DNA
98 <213> ORGANISM: Corynebacterium glutamicum
100 <220> FEATURE:
101 <221> NAME/KEY: CDS
102 <222> LOCATION: (163)..(429)
103 <223> OTHER INFORMATION: ptsH allele
105 <400> SEQUENCE: 3
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108 gagatcgaca ttaaattcccc tcccttgggg ggtttaacta acaaatcgct gcgcccta 120
110 ccgttcggat taacggcgta gcaacacgaa aggacacttt cc atg gct tcc aag 174
111                                     Met Ala Ser Lys
112                                     1
114 act gta acc gtc ggt tcc tcc gtt ggc ctg cac gca cgt cca gca tcc 222
115 Thr Val Thr Val Gly Ser Ser Val Gly Leu His Ala Arg Pro Ala Ser
116   5           10           15           20
118 atc atc gct gaa acg gct gct gag tac gac gac gaa atc ttg ctg acc 270
119 Ile Ile Ala Glu Thr Ala Ala Glu Tyr Asp Asp Glu Ile Leu Leu Thr
120           25           30           35
122 ctg gtt ggc tcc gat gat gac gaa gag acc gac gcg tcc tct tcc ctc 318
123 Leu Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala Ser Ser Ser Leu
124           40           45           50
126 atg atc atg gcg ctg ggc gca gag cac ggc aac gaa gtt acc gtc acc 366
127 Met Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu Val Thr Val Thr
128           55           60           65
130 tcc gac aac gct gaa gct gtt gag aag atc gct gcg ctt atc gca cag 414
131 Ser Asp Asn Ala Glu Ala Val Glu Lys Ile Ala Ala Leu Ile Ala Gln
132           70           75           80
134 gac ctt gac gct gag taaacaacgc tctgcttggt aaaagctcgt tagaagcttg 469
135 Asp Leu Asp Ala Glu
136   85
138 ttaaaagcgg t 480

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141 <210> SEQ ID NO: 4
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143 <212> TYPE: PRT
144 <213> ORGANISM: Corynebacterium glutamicum
146 <400> SEQUENCE: 4
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150 Arg Pro Ala Ser Ile Ile Ala Glu Thr Ala Ala Glu Tyr Asp Asp Glu
151           20           25           30
153 Ile Leu Leu Thr Leu Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala
154           35           40           45
156 Ser Ser Ser Leu Met Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu
157           50           55           60
159 Val Thr Val Thr Ser Asp Asn Ala Glu Ala Val Glu Lys Ile Ala Ala
160   65           70           75           80
162 Leu Ile Ala Gln Asp Leu Asp Ala Glu
163           85
166 <210> SEQ ID NO: 5
167 <211> LENGTH: 20
168 <212> TYPE: DNA
169 <213> ORGANISM: Corynebacterium glutamicum
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Primer ptsHexpl
174 <400> SEQUENCE: 5
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176                                     20
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179 <211> LENGTH: 20
180 <212> TYPE: DNA
181 <213> ORGANISM: Corynebacterium glutamicum
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Primer ptsHexp2
186 <400> SEQUENCE: 6
187 ttctactcagc gtcaaggtcc
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/819,930

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Input Set : A:\Ma278412.app

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